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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=6; day=24; hr=8; min=21; sec=59; ms=301; ]

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Reviewer Comments:

<210> 1

<211> 3846

<212> DNA (BFA4 cDNA)

<213> Homo sapiens

Per 1.823 of the Sequence Rules, the above <212> response is invalid: the only valid <212> responses are just DNA, RNA, or PRT. All explanatory matter (which encompasses "BFA4 cDNA") goes in the <220>-<223> (Feature) section. See below for example:

<220>

<223> BFA4 cDNA

FYI: the above type of error also appears in Sequences 2-6.

<210> 105

<211> 16

<212> PRT

<213> Homo sapiens

<400> 105

Ser Arg Arg His His Cys Arg Ser Lys Ala Lys Arg Ser Arg His His

Please number the above amino acids under every 5 amino acids, starting with "1". Do not insert TAB codes between the amino acid numbers: TABs cause misaligned numbers. Use space characters, instead.

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Application No: 10553137 Version No: 2.0

Input Set:

Output Set:

Started: 2010-06-15 11:26:27.510  
Finished: 2010-06-15 11:26:29.386  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 876 ms  
Total Warnings: 0  
Total Errors: 6  
No. of SeqIDs Defined: 105  
Actual SeqID Count: 105

Error code	Error Description
E 310	Invalid sequence type in <212> in SEQID: (1)
E 310	Invalid sequence type in <212> in SEQID: (2)
E 310	Invalid sequence type in <212> in SEQID: (3)
E 310	Invalid sequence type in <212> in SEQID: (4)
E 310	Invalid sequence type in <212> in SEQID: (5)
E 310	Invalid sequence type in <212> in SEQID: (6)

# SEQUENCE LISTING

<110> Berinstein, Neil  
Gallichan, Scott  
Lovitt, Corey  
Parrington, Mark  
Pedyczak, Artur  
Radvanyi, Laszlo  
Singh-Sandhu, Devender

<120> Tumor Antigens BFA5 for Prevention and/or Treatment of  
Cancer

<130> API-03-03-PCT-US

<140> 10553137

<141> 2010-06-15

<150> PCT/IB2004/001701

<151> 2004-04-15

<150> US 60/462,945

<151> 2003-04-15

<160> 105

<170> PatentIn version 3.2

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<211> 3846

<212> DNA (BFA4 cDNA)

<213> Homo sapiens

<400> 1

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<211> 1281

<212> PRT (BFA4 aa)

<213> Homo sapiens

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Lys Asn Lys Glu Phe Ser Ala Asp Gln Met Ser Glu Asn Thr Asp Gln  
35 40 45

Ser Asp Ala Ala Glu Leu Asn His Lys Glu Glu His Ser Leu His Val  
50 55 60

Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu  
65 70 75 80

Ser Glu Lys Ala Gly Phe Asn Tyr Glu Ser Pro Ser Lys Gly Gly Asn  
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Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala  
100 105 110

Phe Ser Phe Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro  
115 120 125

Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser  
130 135 140

Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala  
145 150 155 160

Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly  
165 170 175

Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp  
180 185 190

Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp  
195 200 205

Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys  
210 215 220

Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile  
225 230 235 240

Lys His Phe Arg Lys Tyr His Leu Gly Leu His Asn Arg Thr Arg Gln  
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Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln  
260 265 270

Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser  
275 280 285

Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly  
290 295 300

Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly  
305 310 315 320

Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys  
325 330 335

Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln  
340 345 350

His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser  
355 360 365

Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro  
370 375 380

Ala Leu Gln Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys  
385 390 395 400

Ile Thr Val Lys Ala Gly Asp Asp Thr Pro Val Gly Tyr Ser Val Pro  
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Ile Lys Pro Leu Asp Ser Ser Arg Gln Asn Gly Thr Glu Ala Thr Ser  
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Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser  
435 440 445

Leu Lys Leu Leu Glu His Tyr Gly Lys Gln His Gly Ala Val Gln Ser  
 450 455 460

Gly Gly Leu Asn Pro Glu Leu Asn Asp Lys Leu Ser Arg Gly Ser Val  
 465 470 475 480

Ile Asn Gln Asn Asp Leu Ala Lys Ser Ser Glu Gly Glu Thr Met Thr  
 485 490 495

Lys Thr Asp Lys Ser Ser Ser Gly Ala Lys Lys Lys Asp Phe Ser Ser  
 500 505 510

Lys Gly Ala Glu Asp Asn Met Val Thr Ser Tyr Asn Cys Gln Phe Cys  
 515 520 525

Asp Phe Arg Tyr Ser Lys Ser His Gly Pro Asp Val Ile Val Val Gly  
 530 535 540

Pro Leu Leu Arg His Tyr Gln Gln Leu His Asn Ile His Lys Cys Thr  
 545 550 555 560

Ile Lys His Cys Pro Phe Cys Pro Arg Gly Leu Cys Ser Pro Glu Lys  
 565 570 575

His Leu Gly Glu Ile Thr Tyr Pro Phe Ala Cys Arg Lys Ser Asn Cys  
 580 585 590

Ser His Cys Ala Leu Leu Leu Leu His Leu Ser Pro Gly Ala Ala Gly  
 595 600 605

Ser Ser Arg Val Lys His Gln Cys His Gln Cys Ser Phe Thr Thr Pro  
 610 615 620

Asp Val Asp Val Leu Leu Phe His Tyr Glu Ser Val His Glu Ser Gln  
 625 630 635 640

Ala Ser Asp Val Lys Gln Glu Ala Asn His Leu Gln Gly Ser Asp Gly  
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Gln Gln Ser Val Lys Glu Ser Lys Glu His Ser Cys Thr Lys Cys Asp  
 660 665 670



Phe Ile Thr Gln Val Glu Glu Glu Ile Ser Arg His Tyr Arg Arg Ala  
675 680 685

His Ser Cys Tyr Lys Cys Arg Gln Cys Ser Phe Thr Ala Ala Asp Thr  
690 695 700

Gln Ser Leu Leu Glu His Phe Asn Thr Val His Cys Gln Glu Gln Asp  
705 710 715 720

Ile Thr Thr Ala Asn Gly Glu Glu Asp Gly His Ala Ile Ser Thr Ile  
725 730 735

Lys Glu Glu Pro Lys Ile Asp Phe Arg Val Tyr Asn Leu Leu Thr Pro  
740 745 750

Asp Ser Lys Met Gly Glu Pro Val Ser Glu Ser Val Val Lys Arg Glu  
755 760 765

Lys Leu Glu Glu Lys Asp Gly Leu Lys Glu Lys Val Trp Thr Glu Ser  
770 775 780

Ser Ser Asp Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu  
785 790 795 800

Arg Gly Ser Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro  
805 810 815

Val Ser Gly Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn  
820 825 830

Val Glu Ala Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu  
835 840 845

Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly  
850 855 860

Ala Leu Pro Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp  
865 870 875 880

Glu Ser Gln Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys  
885 890 895

Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn

900

905

910

Gly Gly Tyr Val Cys Asn Ala Cys Gly Leu Tyr Gln Lys Leu His Ser  
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Thr Pro Arg Pro Leu Asn Ile Ile Lys Gln Asn Asn Gly Glu Gln Ile  
 930 935 940

Ile Arg Arg Arg Thr Arg Lys Arg Leu Asn Pro Glu Ala Leu Gln Ala  
 945 950 955 960

Glu Gln Leu Asn Lys Gln Gln Arg Gly Ser Asn Glu Glu Gln Val Asn  
 965 970 975

Gly Ser Pro Leu Glu Arg Arg Ser Glu Asp His Leu Thr Glu Ser His  
 980 985 990

Gln Arg Glu Ile Pro Leu Pro Ser Leu Ser Lys Tyr Glu Ala Gln Gly  
 995 1000 1005

Ser Leu Thr Lys Ser His Ser Ala Gln Gln Pro Val Leu Val Ser  
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Gln Thr Leu Asp Ile His Lys Arg Met Gln Pro Leu His Ile Gln  
 1025 1030 1035

Ile Lys Ser Pro Gln Glu Ser Thr Gly Asp Pro Gly Asn Ser Ser  
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Gly Ser Pro Ile Glu Lys Tyr Gln Tyr Pro Leu Phe Gly Leu Pro  
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Trp Ser Lys Tyr Lys Leu Ser Val Pro Gly Asn Pro His Tyr Leu  
 1115 1120 1125

Ser His Val Pro Gly Leu Pro Asn Pro Cys Gln Asn Tyr Val Pro  
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Tyr Pro Thr Phe Asn Leu Pro Pro His Phe Ser Ala Val Gly Ser  
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Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys Cys Val  
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His Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu His  
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Met Ser Cys His Gly Asp Ser Gly Pro Phe Gln Cys Ser Ile Cys  
1235 1240 1245

Gln His Leu Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln  
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<212> DNA (BCY1 cDNA)

<213> Homo sapiens

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